

Fig. 1

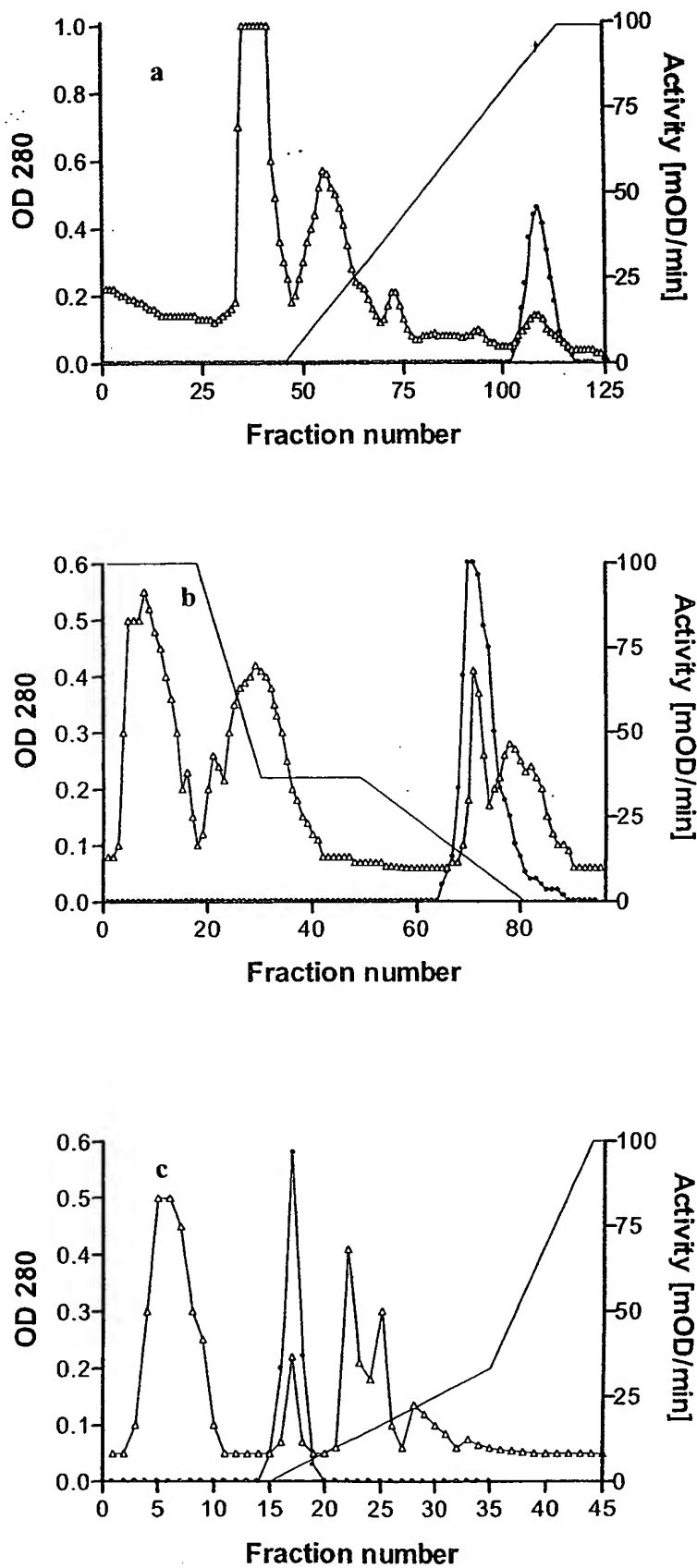
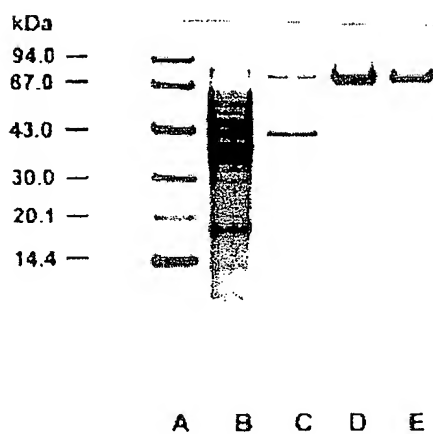


Fig. 2



10008355-10801

Fig. 3

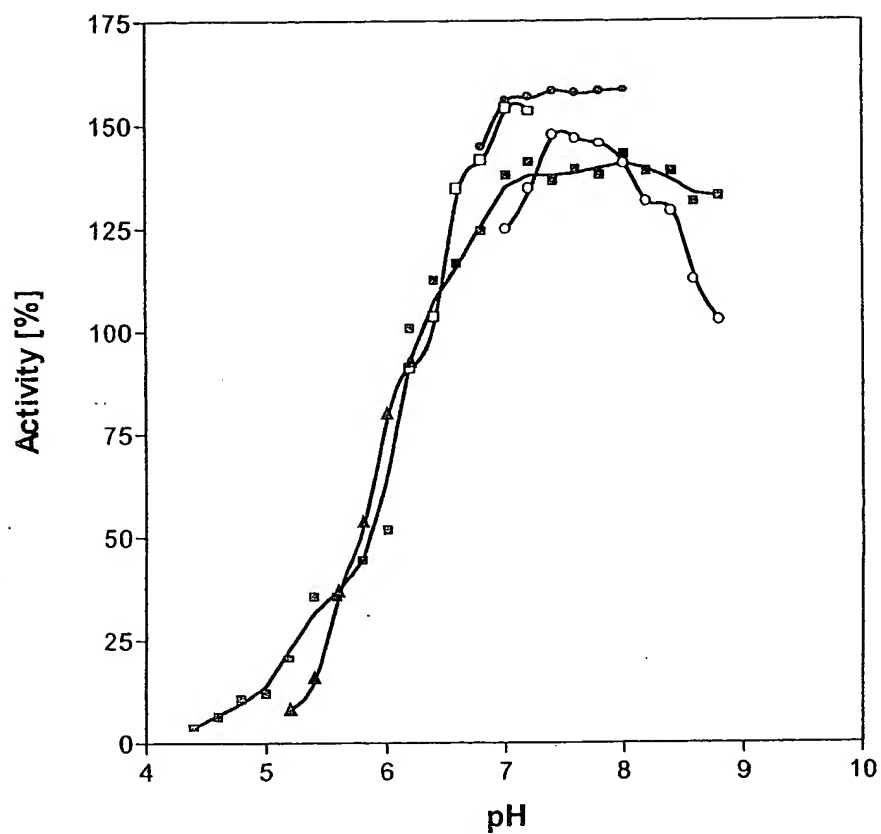


Fig. 4

SEQ ID NO: 1
SEQ ID NO: 2

atgcaaatgaaattaaaaagtattcttctcggagcagccctgctgttgggtgcttcaggggtagccaaagccgacaaagcgatgtggctc 90
M Q M K L K S I L L G A A L L L G A S G V A K A D K G M W L 30
ctcaacgaactcaatcaggagaatctggatcgaatgcgtgagctcggctttacgctcccggttgattcgctctacagtttcgacaagccg 180
L N E L N Q E N L D R M R E L G F T L P L D S L Y S F D K P 60
tccattgccaatgcccgttggttatcttctcgggtggcgatgtaccggtatcacagtgctcgatcagggcctgatctttaccaaccaccactgc 270
S I A N A V V I F G G G C T G I T V S D Q G L I F T N H H C 90
ggataccggtgctatccagagccaaagcacggtggatcacgactatctgcgcgatggtttcgtttctcgcacgatgggtgaggagcttccg 360
G Y G A I Q S Q S T V D H D Y L R D G F V S R T M G E E L P 120
attccgggtctttccgtgaagtatctgcgcaagatcgtgaaggtaacggacaaggtagaaggacagctcaagggatcactgacgagatg 450
I P G L S V K Y L R K I V K V T D K V E G Q L K G I T D E M 150
gagcgtctgcgcaagctcaggaggtatgccagaactggccaaaaaagaaatgcagacgagaaccaactctgcacgttagagcctttc 540
E R L R K A Q E V C Q E L A K K E N A D E N Q L C I V E P F 180
tattccaacaacgaataacttctcctcatcgtctacgatgtattcaaggacgttcgtatggtatttgcctctccagctctgtaggttaagttc 630
Y S N N E Y F L I V Y D V F K D V R M V F A P P S S V G K F 210
ggaggcgataccgacaactggatgtggcgcgctcacacggcgacttcagcgtattccgctgtatgccgggtgccgacaaccggccggcc 720
G G D T D N W M W P R H T G D F S V F R V Y A G A D N R P A 240
gaatacagcaaggacaataaacctataagcccggttacttcgctgcggtatccatgcaaggctacaaggctgacgactatgccatgacc 810
E Y S K D N K P Y K P V Y F A A V S M Q G Y K A D D Y A M T 270
atcggtttcccgggcagtcaggatcgctacctcacttcttgggtgtggaagatcgatcgaaaacgagaacaatcctcgatcgaagtt 900
I G F P G S T D R Y L T S W G V E D R I E N E N N P R I E V 300
cgcggtatcaagcaaggcatctggaaggaagccatgagcgcagatcagcgtaccggtatcaaatatgccagcaagtatgctcagagtgt 990
R G I K Q G I W K E A M S A D Q A T R I K Y A S K Y A Q S A 330
aactattggaagaattcgatcggtatgaaccgcggtctcgtcgtcttgacgtgtaggtcgtaagcgtgccgaggaagagcattcgca 1080
N Y W K N S I G M N R G L A R L D V I G R K R A E E R A F A 360
gactggatccgtaagaacggcaagagtgctgtctatggcgatgtattgtctctctcgcgaaaaggcttataaggaaggagccaaggccaac 1170
D W I R K N G K S A V Y G D V L S S L E K A Y K E G A K A N 390
cgtgagatgacttatttgagcgagacgctcttcgggtggtaccgaggtggttcgttttgacagtttgccaacgcattggctacaaatcct 1260
R E M T Y L S E T L F G G T E V V R F A Q F A N A L A T N P 420
gatgctatgcgggtatcctcaaatcgcttgacgacaagtacaaagactacctccctcgctcgacgcgtaaggtgctgcccgcacatgctc 1350
D A H A G I L K S L D D K Y K D Y L P S L D R K V L P A M L 450
gatattgtacgcccgcgtatccctgcccagacaagctccccgatattcaagaatgtaatcgacaagaaattcaaggcgacacgaagaag 1440
D I V R R R I P A D K L P D I F K N V I D K K F K G D T K K 480
tatgcagactcgtatttcgacaagagtggttgccttatagcgacaagttccatgccatgctcaagtcctggacaaggaaaagtttgcc 1530
Y A D F V F D K S V V P Y S D K F H A M L K S M D K E K F A 510
aaggctatcgagaaagatccggcagtagagctttccaagagcgtaatagctgctgctcgcgctattcagggcgtgctgagtgccaatgcc 1620
K A I E K D P A V E L S K S V I A A A R A I Q A D A M A N A 540
tatgccattgagaagggaagcgtcttttcttgcgggttgctgagatgtaccgccgagctgctctgcgcgagcgtgccaacttcacc 1710
Y A I E K G K R L F F A G L R E M Y P G R A L P S D A N F T 570
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M R M S Y G S I K G Y E P Q D G A W Y N Y H T T G K G V L E 600
aagcaggtatcctaagagcgatgagtttgccgtacaggagaatatcctcgacctcttcgcacacaaaactatggtcgctatgccgagaac 1890
K Q D P K S D E F A V Q E N I L D L F R T K N Y G R Y A E N 630
ggtcagctccatcgctttcctatcgacaacacgacatcacggggcggttaactccggtagcccggtattcgataagaacggcgctctgatc 1980
G Q L H I A F L S N N D I T G G N S G S P V F D K N G R L I 660
ggctcttgccttcgatggcaactgggaagctatgagtggtgacatcgagttcgaaacccgatctgcagcgacacatcagcgtggacatccgc 2070
G L A F D G N W E A M S G D I E F E P D L Q R T I S V D I R 690
taegttctcttcattgattgacaaaagggtcagtgccccgctctcatccaagagctgaagttgatctaa 2139
Y V L F M I D K W G Q C P R L I Q E L K L I * 713

10008355-110801

Fig. 5

103011-5580001

~~SEQ ID NO: 3~~ DPP-7
~~SEQ ID NO: 4~~ V-8

644 TGGNSGSPVFDKNGRLIGLAFDGNWEAMSGDIEFPDLQRTISVDIRYVLFM695
TGGNSGSPVF++ +IG+ + G +G + ++ + +I + F
704 TGGNSGSPVFNEKNEVIGIHWGGVPNEFNCAVFINENVRNFLKQNIEDIHFA863

Fig. 6

108011-55630001

SEQ ID NO: 5 S1 1 MASQALGFLHONGINTYKKWLTISVAAASFAASHADEGMOPHOLP-AMADVTKAKGTEIDAKSISKTEHPMN--AVEST
SEQ ID NO: 6 S2 1 -----MRLMAALYLTCTGATADGOMOPOLP-SLADKISAREGIDIPADKADLISYPMN--AVGCL
SEQ ID NO: 7 X 1 -----MRLNLTSTSVLATTITVDSTHAGEGMMPOLP-ELAGPLKQAGLOTSPQLSNLGDYGC--AVVSL
SEQ ID NO: 8 P1 1 -----MOMKLSITIGALIHGASGVAAKDGWMLDNLNENIDRARELEFTPLDLSYSEDKPSLANAVYEG
SEQ ID NO: 9 P2 1 -----MKRLHLPFAVLCLOLAHDEGMWVQOLG-RKYAQMKERGLKKEYDINPNGTSLKDAVYVLT
S1 78 GCCTASVSPKGLVNTNHCAGVSGIQNSTPEKNTLQDGEIAKTEDELPAAPGSRVYVTEGVNVTERRVKGLENKGTG-
S2 62 GCTASVSPKGLVNTNHCAGVSGIQNSTPEKNTLQDGEIAKTEDELPAAPGSRVYVTEGVNVTERRVKGLENKGTG-
X 66 GCTASVSPKGLVNTNHCAGVSGIQNSTPEKNTLQDGEIAKTEDELPAAPGSRVYVTEGVNVTERRVKGLENKGTG-
P1 71 GCCTGITSVSDQGLIETNHHCGVCAIOSQSTVPHDYLRDGEVSRVNG-DELPPIGLSVKYLKIVKVTDKVEGOLKGTID-
P2 67 GCCTGITSVSDQGLIETNHHCGVCAIOSQSTVPHDYLRDGEVSRVNG-DELPPIGLSVKYLKIVKVTDKVEGOLKGTID-
S1 157 -----RELYQGVENOEKALVAECERDEGRCQVYSHGTEENLYKQLETRDYRLVYNPAGSVGKKGEDYDNMMMPRH
S2 140 -----LKRYEELIENHSHKALIKSCAADNYRONVRSHEHGLEKMLKQMDIRDYRLVYAPPSVGGYGGIDINDYEPHSH
X 146 -----PKRTTALETESKQELAKCEEQGRCCFESAGNTIRYKNEIKDYRLVYAPQCSVGKKGEDYDNMMMPRH
P1 149 -----EMERLRKAEVCEELAKENADENOLCIVEPYSNNEVELTVYDVKDYRVYEAPESSVGKKGEDYDNMMMPRH
P2 146 NSMDYLSPKYLOKLADKAKGNSAKNPELSVELKAYGENLYMTKTYTDVRLVCAPISTICKGADTDNMTMPRH
S1 231 GDYSERAVYVSKNGKPAEFADNPYEPKSEIKVSAKGVSEGEVNAVAGYPCGRITRYRLATEVONEHEMAPEKQTLER
S2 214 GDFATIRAVYVKGDKGPAEFSEDNIPYTPKSYLAKVNADGWKAGDGVNAVAGYPCGRITRYRLATEVONEHEMAPEKQTLER
X 221 GDFSEYRAVYVKGDKGPAEFSEDNIPYTPKSYLAKVNADGWKAGDGVNAVAGYPCGRITRYRLATEVONEHEMAPEKQTLER
P1 224 GDFSEYRAVYVKGDKGPAEFSEDNIPYTPKSYLAKVNADGWKAGDGVNAVAGYPCGRITRYRLATEVONEHEMAPEKQTLER
P2 226 GDFSEYRAVYVKGDKGPAEFSEDNIPYTPKSYLAKVNADGWKAGDGVNAVAGYPCGRITRYRLATEVONEHEMAPEKQTLER
S1 311 FIEIIRKATAPEGSDERIKYESOTACLANVAKNTSMETFGKSTVMDRKLAEKLAETWAKDS---REAKYGTIAET
S2 294 QIDTIEAMGQKADDAIKVAGNMAAMAKKNGELAGKATDYGIKQRENDIETAVLTKNPN-----INONLISEI
X 301 LIALIEAASKONPDIOVKVASTIAGLNTSKNTDGLDGERINAGQKQSEETAVLAKQOGLI---RGHEALAAHQTL
P1 304 KQGIWKEAMSAADQATRIKVASKVAOSANNYKNSIGANRGELARDVIGRKRAEERAFADVIRKNGKSAV---YGDVLSSTE
P2 306 RQGVMLREMLADPQIKIMYSAKVNASQNAVYKRAIGANWAKTRGIRONKOMODRIWAGAKOQTP-----RYEAVVHE
S1 388 DALIAKSKAHOERDMITSYISSTVMPPTANNLYRLAHEKOLPMQOREPEFODRDVTRFKASVERIDIRRYAASVDKAVLTQ
S2 368 EVLLAEQOLQOTQNTYFTNAOSSSTITLANNLYRLAKEKOKSDAEREIGQOERDIAFESSRIKRIIDSSEDAVKDTMTQ
X 378 VDLTEQYKANODRDEVLGOENGSGVIGVAVNLRLAETRTKSDQREAGQOERDPTIEGNLQOMERPLPEYDROQOY
P1 381 KAYKEGAKANRENTYSETLFGTEVVRFAQFANALATNPDAHAGIKSIDKQDYLPSIDRKVLPAMDIVRRPLPAD
P2 380 IDATVAKRADLRRYMYIEGIRGIEFARSPITPDETKALQENDASPRKEAIDKIRTRYSEKANKOYSAEVDKKVAVA
S1 468 MLKRYAALPEAQRIIPAMDRAFGIDNKVNEAKAKTIDKMYAKTELGKNDVRLAMMEKSVDDKASIKDPTIOEAVAMMDTN
S2 448 DIN--AYLSQPNRWALDNLNDKNI--VSLAAKIDGLSYITLITDQORLAWMEADAKABETSSDPPIRLAVALLDITN

108011-5530001

X 458 WLEKNTLPVKORVAIDVWEDGIPAT-----L-KRLGDKLSSSEERKMNDRAPAESODPAIRVAVAPAL
P1 461 KLPDIKRVNDKDEKGTTRKYADFEVD--KS-----VVPYSDKTHANLKSNDKEKPAKAEKDPAYELSKSYLAA
P2 460 MLETKELKEIPYENTPLHRLTKDRFAG---DVQAYVDIDFARSVEGSAQFDARAVPSVEKLAEDAVLPASSVADY
S1 548 NSEKKEKELDCELMKVRPOMDNTALNLECKEPYADANSIRVYCHVKYSPKDCIYAVPTPLTEGVCODNG-ID
S2 524 NAOEKAETKILAGKISTARPAVMAVIDYKANNWPYPDANCITRISYGVWDGYOSRDNTYKOPETRIKDGIAKHNG-VZ
X 530 EETERONKIRITGELEKARBIYLCATADYKNSHCKEYVPDANSIRITTECHVKYSPKDCIYAVPTPLTEGVCODNG-VZ
P1 530 RAICADAMANAYAEKGRLEAGLEBENTP--GRALPSDANETMRMSYCSLEKYEPPDCAYVYNYHUTGKGVLEKODPKSD
P2 536 RQTYNELRPYDDPILRAQRTYELAGLLEMG--DODLEPDANIILRETYGVKGYSPRDNVZAGHOUWLDGVLEKEDPDNV
S1 627 PEDAPKQOLETHIKOKYGDLYMKSDS-----VPVNTLSIEDITGNSGSPITNGRABIVGILB
S2 603 PYNAPKQILDALISVOREGDHLVKSYYODPRGWI CRLFSCLDKPEEFNSVPVNTLSYDITGNSGSPVBNKGELVGLNB
X 609 PEDSPKSLINAIKAKSYANTADORIGT-----VPVNTLSIDITGNSGSPVLDAGKIVGLAB
P1 608 EFAVOENILDTFRKNGYGRVANGOLH-----LAF--LSNNDITGNSGSPVJDKNGRLIGLAB
P2 614 ELEVDPKIKAVYERKDEGRVADRSGRMP-----VAFQNTHTTIGNSGSPVANNANGELIGLNB
S1 686 DGVYESITIGCMAFDNEINRSIHVDSRVMTVMVKYLDHNDNTLAEMEIVN-
S2 683 DSTYEATIKDMEBNPTITRAVHVHDIRYILMMNDEVDHADNTLEKELDIWRN
X 668 DGNWESVSNNWVEDPVMTRIIANDSRVYQWIMTEYAPAPHLKEELNITYR-
P1 665 DGNWEAMSGLIEEPDLQRTISVDIRYVLEFMDIKW-----
P2 672 DRNWEVGVDIOYADYORSIIVDIRYVLEVIDKVGCCORLIDEMNIVP-